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Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=4; day=25; hr=14; min=3; sec=3; ms=423;]

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Application No: 10539962

Version No: 1.0

Input Set:

Output Set:

Started: 2008-04-14 16:27:59.858

Finished: 2008-04-14 16:28:01.311

Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 453 ms

Total Warnings: 20

Total Errors: 0

No. of SeqIDs Defined: 37

Actual SeqID Count: 37

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
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W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
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W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (36)
W 213	Artificial or Unknown found in <213> in SEQ ID (37)

Input Set:

Output Set:

Started: 2008-04-14 16:27:59.858
Finished: 2008-04-14 16:28:01.311
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 453 ms
Total Warnings: 20
Total Errors: 0
No. of SeqIDs Defined: 37
Actual SeqID Count: 37

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> FAGAN, RICHARD JOSEPH
 PHELPS, CHRISTOPHER BENJAMIN
 RODRIGUES, TANIA MARIA
 POWER, CHRISTINE
 DE TIANI, MARIATELLA

<120> SPLICE VARIANT OF HUMAN PLACENTAL GROWTH HORMONE

<130> C&R-106

<140> 10539962

<141> 2008-04-14

<150> PCT/GB03/05594

<151> 2003-12-19

<150> GB 0229850.3

<151> 2002-12-20

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		20					25					30			

Asp	Asn	Ala	Met	Leu	Arg	Ala	Arg	Arg	Leu	Tyr	Gln	Leu	Ala	Tyr	Asp
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<212> PRT

<213> Homo sapiens

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20 25 30

Asp Asn Ala Met Leu Arg Ala Arg Arg Leu Tyr Gln Leu Ala Tyr Asp
35 40 45

Thr Tyr Gln Glu Phe Val Ser Ser Trp Val Met Glu Ser Ile Pro Thr
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Pro Ser Asn Arg Val Lys Thr Gln Gln Lys Ser
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20 25 30

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35 40 45

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50 55 60

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Ser Ile Pro Thr Pro Ser Asn Arg Val Lys Thr Gln Gln Lys Ser Asn
65 70 75 80

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Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu
85 90 95

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Pro Val Gln Leu Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly
100 105 110

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Ala Ser Asp Ser Asn Val Tyr Arg His Leu Lys Asp Leu Glu Glu Gly
115 120 125

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Ile Gln Thr Leu Met Trp Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly
130 135 140

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Gln Ile Phe Asn Gln Ser Tyr Ser Lys Phe Asp Thr Lys Ser His Asn
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ccaacacctt ccaacagggt gaaaacgcag cagaaatcta acctagagct gctccgcata 180
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<213> Homo sapiens

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Ala Arg Arg Leu Tyr Gln Leu Ala Tyr Asp Thr Tyr Gln Glu Phe Val
          20          25          30

Ser Ser Trp Val Met Glu Ser Ile Pro Thr Pro Ser Asn Arg Val Lys
          35          40          45

Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu
          50          55          60

Ile Gln Ser Trp Leu Glu Pro Val Gln Leu Leu Arg Ser Val Phe Ala
65          70          75          80

Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Arg His Leu
          85          90          95

Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Trp Arg Leu Glu Asp
          100          105          110

Gly Ser Pro Arg Thr Gly Gln Ile Phe Asn Gln Ser Tyr Ser Lys Phe
          115          120          125

Asp Thr Lys Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu
          130          135          140

Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg
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Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
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<211>	38	
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20 25 30

Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala Arg Arg Leu Tyr Gln
35 40 45

Leu Ala Tyr Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Leu Lys
50 55 60

Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe
65 70 75 80

Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Val Lys Thr Gln Gln Lys
85 90 95

Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp
100 105 110

Leu Glu Pro Val Gln Leu Leu Arg Ser Val Phe Ala Asn Ser Leu Val
115 120 125

Tyr Gly Ala Ser Asp Ser Asn Val Tyr Arg His Leu Lys Asp Leu Glu
130 135 140

Glu Gly Ile Gln Thr Leu Met Trp Arg Leu Glu Asp Gly Ser Pro Arg
145 150 155 160

Thr Gly Gln Ile Phe Asn Gln Ser Tyr Ser Lys Phe Asp Thr Lys Ser
165 170 175

His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe
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Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys
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Arg Ser Val Glu Gly Ser Cys Gly Phe
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Cys Leu Ser Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu
20 25 30

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Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala Arg Arg Leu Tyr Gln

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Leu Ala Tyr Asp Thr Tyr Gln Glu Phe Val Ser Ser Trp Val Met Glu			
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tct att cca aca cct tcc aac agg gtg aaa acg cag cag aaa tct aac			240
Ser Ile Pro Thr Pro Ser Asn Arg Val Lys Thr Gln Gln Lys Ser Asn			
65	70	75	80
cta gag ctg ctc cgc atc tcc ctg ctg ctc atc cag tca tgg ctg gag			288
Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu			
	85	90	95
ccc gtg cag ctc ctc agg agc gtc ttc gcc aac agc ctg gtg tat ggc			336
Pro Val Gln Leu Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly			
	100	105	110
gcc tcg gac agc aac gtc tat cgc cac ctg aag gac cta gag gaa ggc			384
Ala Ser Asp Ser Asn Val Tyr Arg His Leu Lys Asp Leu Glu Glu Gly			
	115	120	125
atc caa acg ctg atg tgg agg ctg gaa gat ggc agc ccc cgg act ggg			432
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Gln Ile Phe Asn Gln Ser Tyr Ser Lys Phe Asp Thr Lys Ser His Asn			
145	150	155	160
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Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys			
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195			

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catgacgcac tgctcaagaa ctacgggctg ctccactgct tcaggaagga catggacaag	540
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